GenePattern

HeatMapViewer Documentation

Module name: HeatMapViewer
Description: Displays a heat map
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Summary:
The HeatMapViewer module displays expression values in a heat map format where the largest values are displayed as the reddest (hot), the smallest values are displayed as the bluest (cool), and intermediate values are a lighter color of either blue or red. This is a very convenient way to display three-dimensional data (samples, features, and expression values).

Display Options
There are a number of options controlling the appearance of the heat map that can be set by selecting the *Display Options* item in the *Edit* menu. You can choose between radio buttons for *Relative* and *Global* color schemes. The relative choice causes the colors for expression values to be scaled as a function of the number of standard deviations relative to the mean for each row. The global choice scales values using the minimum and maximum values in the entire dataset. To display the color legend, select the *Legend* item from the *View* menu. You can choose whether to show or hide row names and descriptions and column names from the display by deselecting the corresponding check box. The grid size slider controls the size of each element in the heat map. The show grid checkbox controls whether a grid is drawn around each element.

Saving Images
Users can save the color gram image to a file by selecting *File>Save Image*. Choices for the output file format are bmp, jpeg, png, and tiff.

Finding Features
To find a feature in the heatmap, select *Edit>Find*. You can choose whether to match the case of the text you're searching for by selecting the *Match case* checkbox at the bottom of the find dialog.

Expression Profiles
The expression profile for a feature plots expression value per sample.
To display an expression profile:
1. Select one or more features.

2. Click *View>Profile*. Alternatively, right-click and select *Profile* from the context menu.

Saving Datasets
You can use the viewer to create a new dataset.

1. Select *File>Save Dataset*. A window appears.
2. Choose the features and samples to include in the dataset by selecting the features and sample names in the viewer.
3. Choose a location and name for the new dataset.
4. Click *Save* to save the new dataset.

Annotations

The viewer provides two annotation methods:

- Feature and sample annotations use color to annotate features and samples in the heatmap

- GeneCruiser annotations retrieve information about Affymetrix probe ids and adds it to the feature table

To use feature annotations:
1. Create a feature list file.

2. Select *File>Open Feature List(s)* to open your feature list file. In the Feature column of the feature table, a color bar appears next to each feature in the feature list.

3. Select E*dit>Feature Annotations* to edit the color or close the feature list:
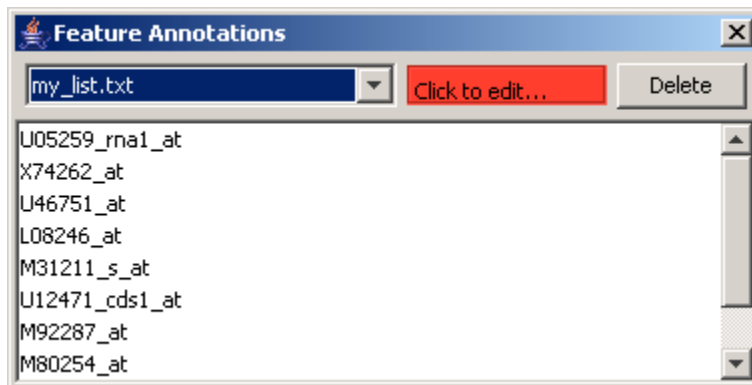
4. In the Feature Annotations window, select your feature list from the drop-down list. The color assigned to that feature list appears in the box to the right.

- To change the color, click the box and select a new color.

- To close the feature list and remove the color bars from the table, click *Delete*.

To use sample annotations:
1. Create a cls file.
2. Select *File>Open Cls File* to open your cls file. A color bar appears below each sample name.
3. Edit and delete sample annotations as described above for feature annotations

To use GeneCruiser annotations:
1. Select *GeneCruiser>Gene Information*.

2. Select the features that you want to retrieve annotations for in the table.

3. Choose which fields to retrieve from GeneCruiser in the GeneCruiser dialog.

4. The annotations appear in additional columns in the table.

Parameters

dataset.filename	The dataset to display - .gct, .res, odf type=Dataset

Platform Dependencies
CPU Type: any
OS: any
Language: Java
Java JVM Level: 1.4